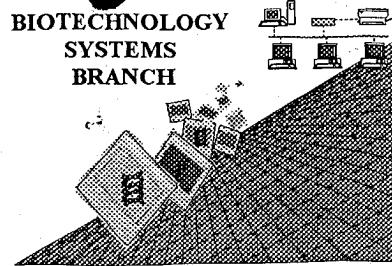


*MTH*

## RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/823,649

Source: OPE

Date Processed by STIC: 4/20/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/823,649</u>
<b>ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE</b>		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: <b>(2) INFORMATION FOR SEQ ID NO:X:</b> <b>(i) SEQUENCE CHARACTERISTICS:</b> (Do not insert any headings under "SEQUENCE CHARACTERISTICS") <b>(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:</b> <b>This sequence is intentionally skipped</b>  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <b>&lt;210&gt; sequence id number</b> <b>&lt;400&gt; sequence id number</b> <b>000</b>	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input checked="" type="checkbox"/> Use of "Artificial" (NEW RULES)	Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) _____ are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/823,649

DATE: 04/20/2001  
TIME: 07:42:37

Input Set : A:\RPA1006.ST25.txt  
Output Set: N:\CRF3\04202001\I823649.raw

3 <110> APPLICANT: Smith, Edward  
 4 Elfstrom, Carita  
 5 Gelfand, David  
 6 Higuchi, Russell  
 7 Myers, Thomas  
 8 Schoenbrunner, Nancy  
 9 Wang, Alice  
 11 <120> TITLE OF INVENTION: HIGH TEMPERATURE REVERSE TRANSCRIPTION USING MUTANT DNA POLYMERASES  
 13 <130> FILE REFERENCE: RPA1006  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/823,649  
 C--> 15 <141> CURRENT FILING DATE: 2001-03-30  
 15 <150> PRIOR APPLICATION NUMBER: US 60/198,336  
 16 <151> PRIOR FILING DATE: 2000-04-18  
 18 <160> NUMBER OF SEQ ID NOS: 21  
 20 <170> SOFTWARE: PatentIn version 3.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 11  
 24 <212> TYPE: PRT  
 C--> 25 <213> ORGANISM: Artificial *see item 11 in Exam Summary Sheet*  
 27 <220> FEATURE:  
 28 <223> OTHER INFORMATION: sequence motif  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: VARIANT  
 32 <222> LOCATION: (2)...(2)  
 33 <223> OTHER INFORMATION: X is S or A  
 36 <220> FEATURE:  
 37 <221> NAME/KEY: VARIANT  
 38 <222> LOCATION: (3)...(3)  
 39 <223> OTHER INFORMATION: X is any amino acid  
 42 <220> FEATURE:  
 43 <221> NAME/KEY: VARIANT  
 44 <222> LOCATION: (4)...(4)  
 45 <223> OTHER INFORMATION: X is any amino acid  
 48 <220> FEATURE:  
 49 <221> NAME/KEY: VARIANT  
 50 <222> LOCATION: (5)...(5)  
 51 <223> OTHER INFORMATION: X is L or I  
 54 <220> FEATURE:  
 55 <221> NAME/KEY: VARIANT  
 56 <222> LOCATION: (6)...(6)  
 57 <223> OTHER INFORMATION: X is any amino acid  
 60 <220> FEATURE:  
 61 <221> NAME/KEY: VARIANT  
 62 <222> LOCATION: (7)...(7)  
 63 <223> OTHER INFORMATION: X is any amino acid  
 66 <220> FEATURE:  
 67 <221> NAME/KEY: VARIANT

Does Not Comply  
Corrected Diskette Needed

pp 1-3,5

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/823,649

DATE: 04/20/2001  
TIME: 07:42:37

Input Set : A:\RPA1006.ST25.txt  
Output Set: N:\CRF3\04202001\I823649.raw

68 <222> LOCATION: (8)..(8)  
 69 <223> OTHER INFORMATION: X is any amino acid  
 72 <220> FEATURE:  
 73 <221> NAME/KEY: VARIANT  
 74 <222> LOCATION: (9)..(9)  
 75 <223> OTHER INFORMATION: X is any amino acid  
 78 <220> FEATURE:  
 79 <221> NAME/KEY: VARIANT  
 80 <222> LOCATION: (10)..(10)  
 81 <223> OTHER INFORMATION: X is any amino acid  
 84 <400> SEQUENCE: 1  
 86 Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Glu  
 87 1 5 10  
 89 <210> SEQ ID NO: 2  
 90 <211> LENGTH: 11  
 91 <212> TYPE: PRT  
 C--> 92 <213> ORGANISM: Artificial item 11  
 94 <220> FEATURE:  
 95 <223> OTHER INFORMATION: sequence motif  
 97 <220> FEATURE:  
 98 <221> NAME/KEY: VARIANT  
 99 <222> LOCATION: (3)..(3)  
 100 <223> OTHER INFORMATION: X is Q or G  
 103 <220> FEATURE:  
 104 <221> NAME/KEY: VARIANT  
 105 <222> LOCATION: (6)..(6)  
 106 <223> OTHER INFORMATION: X is S or A  
 109 <400> SEQUENCE: 2  
 111 Leu Ser Xaa Glu Leu Xaa Ile Pro Tyr Glu Glu  
 112 1 5 10  
 114 <210> SEQ ID NO: 3  
 115 <211> LENGTH: 11  
 116 <212> TYPE: PRT  
 C--> 117 <213> ORGANISM: Artificial  
 119 <220> FEATURE:  
 120 <223> OTHER INFORMATION: sequence motif  
 122 <400> SEQUENCE: 3  
 124 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 125 1 5 10  
 127 <210> SEQ ID NO: 4  
 128 <211> LENGTH: 11  
 129 <212> TYPE: PRT  
 C--> 130 <213> ORGANISM: Artificial  
 132 <220> FEATURE:  
 133 <223> OTHER INFORMATION: sequence motif  
 135 <220> FEATURE:  
 136 <221> NAME/KEY: VARIANT  
 137 <222> LOCATION: (3)..(3)  
 138 <223> OTHER INFORMATION: X is Q or G

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/823,649

DATE: 04/20/2001  
TIME: 07:42:37

Input Set : A:\RPA1006.ST25.txt  
Output Set: N:\CRF3\04202001\I823649.raw

W-OK 141 <400> SEQUENCE: 4  
143 Leu Ser Xaa Glu Leu Ser Ile Pro Tyr Glu Glu  
144 1 5 10  
146 <210> SEQ ID NO: 5  
147 <211> LENGTH: 11  
148 <212> TYPE: PRT  
C--> 149 <213> ORGANISM: Artificial  
151 <220> FEATURE:  
152 <223> OTHER INFORMATION: sequence motif  
154 <220> FEATURE:  
155 <221> NAME/KEY: VARIANT  
156 <222> LOCATION: (7)..(7)  
157 <223> OTHER INFORMATION: X is V or I  
160 <400> SEQUENCE: 5  
W-OK 162 Leu Ser Val Arg Leu Gly Xaa Pro Val Lys Glu  
163 1 5 10  
165 <210> SEQ ID NO: 6  
166 <211> LENGTH: 11  
167 <212> TYPE: PRT  
C--> 168 <213> ORGANISM: Artificial  
170 <220> FEATURE:  
171 <223> OTHER INFORMATION: sequence motif  
173 <400> SEQUENCE: 6  
175 Leu Ser Lys Arg Ile Gly Leu Ser Val Ser Glu  
176 1 5 10  
178 <210> SEQ ID NO: 7  
179 <211> LENGTH: 11  
180 <212> TYPE: PRT  
C--> 181 <213> ORGANISM: Artificial  
183 <220> FEATURE:  
184 <223> OTHER INFORMATION: sequence motif  
186 <220> FEATURE:  
187 <221> NAME/KEY: VARIANT  
188 <222> LOCATION: (8)..(8)  
189 <223> OTHER INFORMATION: X is S or T  
192 <400> SEQUENCE: 7  
W-OK 194 Leu Ala Gln Asn Leu Asn Ile Xaa Arg Lys Glu  
195 1 5 10  
197 <210> SEQ ID NO: 8  
198 <211> LENGTH: 11  
199 <212> TYPE: PRT  
200 <213> ORGANISM: Thermus aquaticus  
202 <400> SEQUENCE: 8  
204 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
205 1 5 10  
207 <210> SEQ ID NO: 9  
208 <211> LENGTH: 11  
209 <212> TYPE: PRT  
210 <213> ORGANISM: Thermus flavus